

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 1

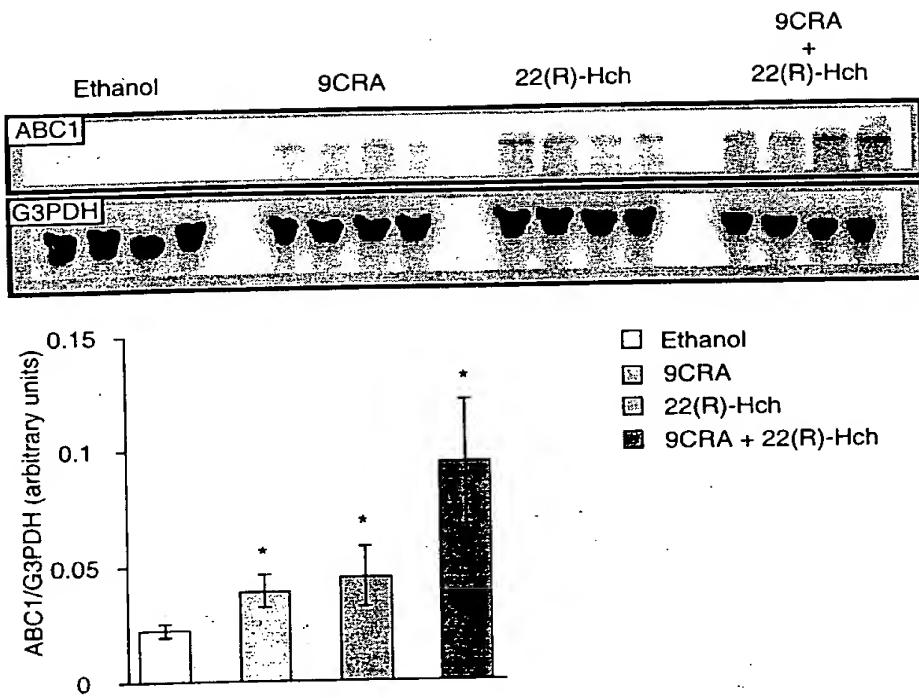


FIG. 2A

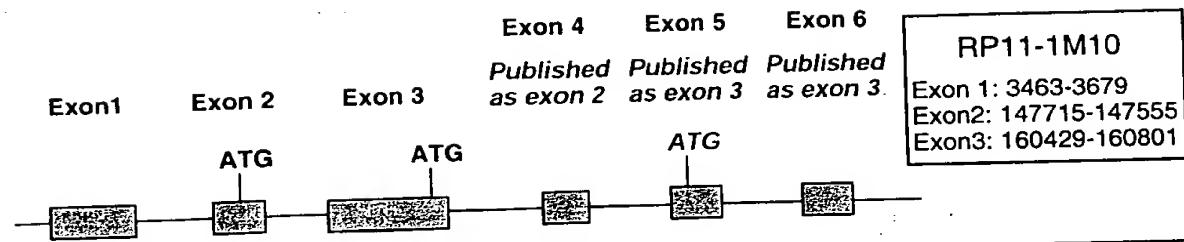


FIG. 2B

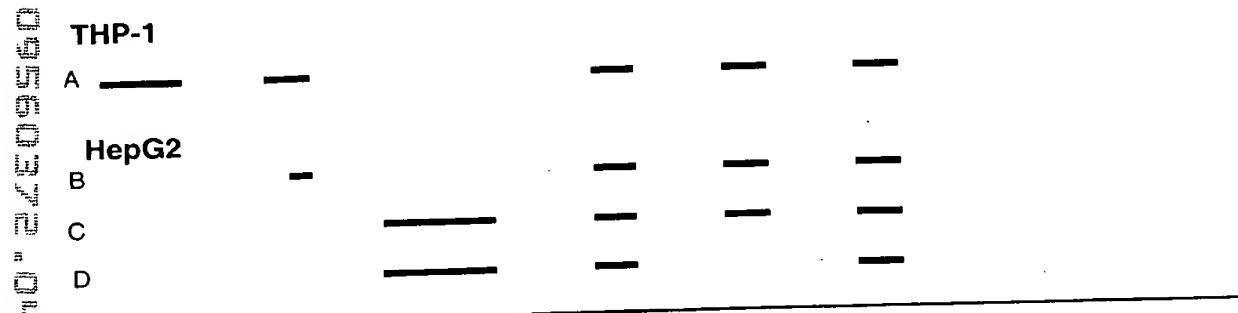


FIG. 2C

1

22

61

A, B MACWPQLRVLLWKNLTFRQQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAM  
C, D MCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAM

tBlastn result: Alignment between hABC1 and hABCR .  
Identical = 32/56 (57%), conservative = 12/56 (21%)

• Blastn result: Alignment between hABC1 and hABC3.

Identical = 20/44 (45%), conservative = 7/44 (16%)

Identical = 26/44 (59%), Conserved = 33/44 (75%)

<b>hABC1</b> <pre>1MACWPQLRVLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL 44     -        - -   -    -        -   </pre>	<b>hABC3</b> <pre>1MAVLROLALLWKNYTLQKRKVLVTVLELFPLLFGSILIWRL 44</pre>
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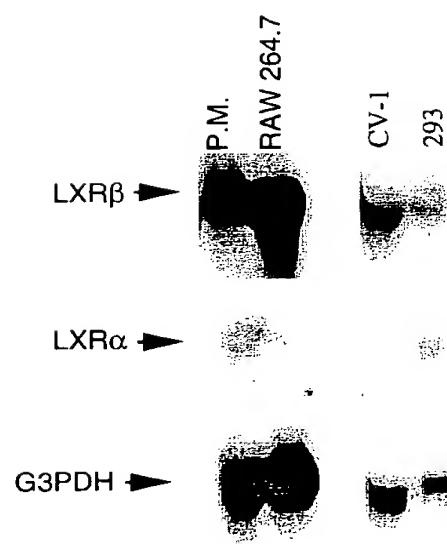
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FIG. 3

acctgagtttggccagaataaggtagacatttagtttgtggcttgatggatgacttaaatatttagacatalggtg  
CREBP1CJUN  
tgtaggccctgcattccactcttgccttttttgcggccctccagtgtttggtagtttgcctccctacagccaaagg  
-928bp  
caaacagataagttggaggctggagtggtacataatttacacgactgcaattctctggctgcacttcacaa  
atgtatacaactaaatacaagtccctgtgttttacacagggaggctgtcaatataatgaaattaaaagggg  
CEBPB  
gctggtccatattgttctgtgtttttgtttttttttttgtggccctcccttcattatgaagagaagc  
HNF3B IRF1  
agtaagatgttcctctcggtccctgaggacctggggagctcaggctgggaatctccaaggcagttaggtc  
NF-KB  
gcctatcaaaaatcaaagtccaggttgtggggggaaaacaaaagcagcccattacccagaggactgtcc  
gcctccctcaccctcagccctaggcctttaggcttggaaaggaaacaaaagacaagacaaaatgatggcgtctgag  
ggagattcagcctagagctctctcccaatccctccctccggctgaggaaactaacaaggaaaaaaa  
Sac1  
attgcggaaagcaggatttagagaaagcaattccactggtgccttggctgccggaaacgtggactagag  
Stat1  
agtctgcggcgcagccccagccctaggcgttcccgccgtttaggcccggccggccggccggccgg  
ggacgcagaccgcggaccctaagacacacctgtgtaccctccaccccccacccacccacccatcccccaa  
ctccctagatgtcgctggcgctgaacgtcccgttaagggcgccggccggctccacgtgcctctgct  
MYCMAX  
gagtgtactgaactacataaacagaggccggaaacggggcgggaggaggagagcacaggcttgac  
AP1 SP1  
cgatagtaacctctgcgtcggtcagccgaatcTATAAagaacttagtcccggcaaaaacccgtaa  
ttgcgagcgagagtgagtggggccgggaccctcagagccgagccgaccctctccggctg  
+101  
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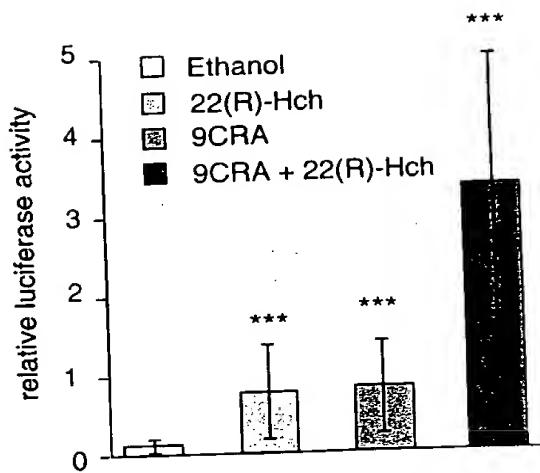
FIG. 4



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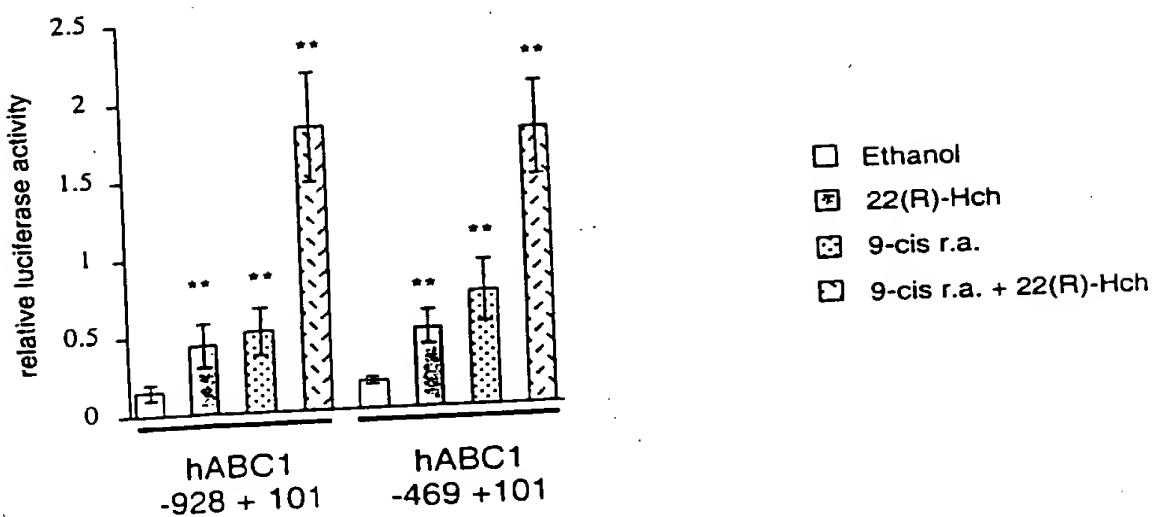
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FIG. 5A



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FIG. 5B



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FIG. 5C

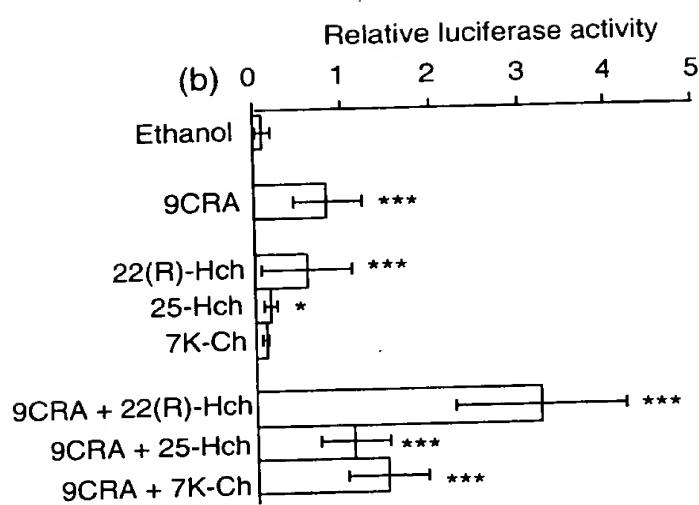


FIG. 6A

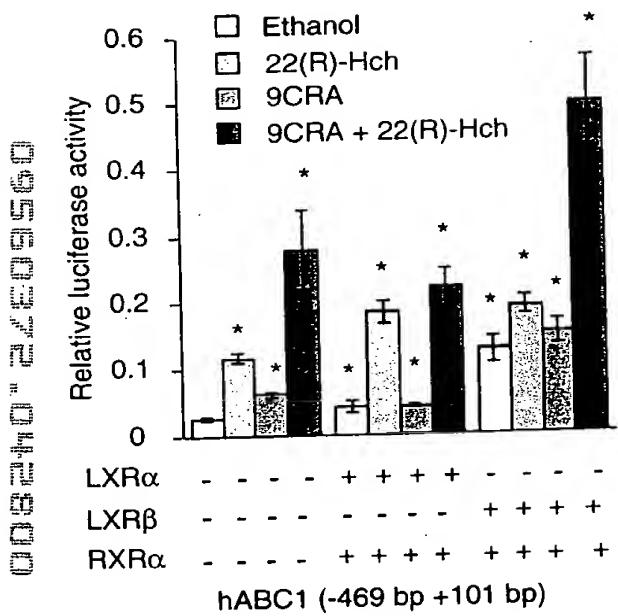
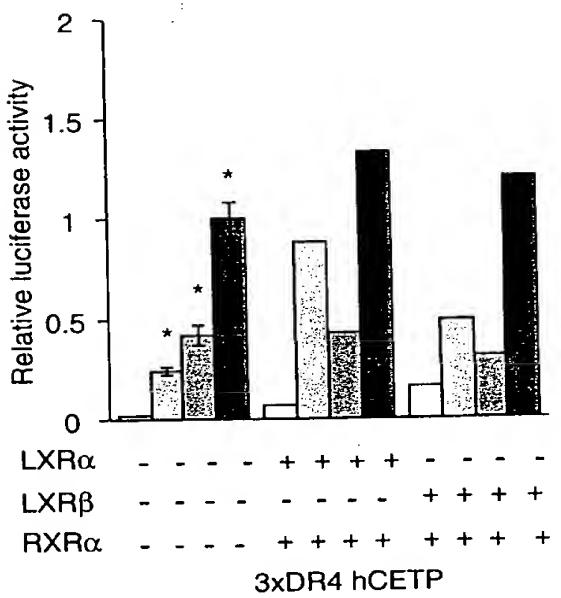
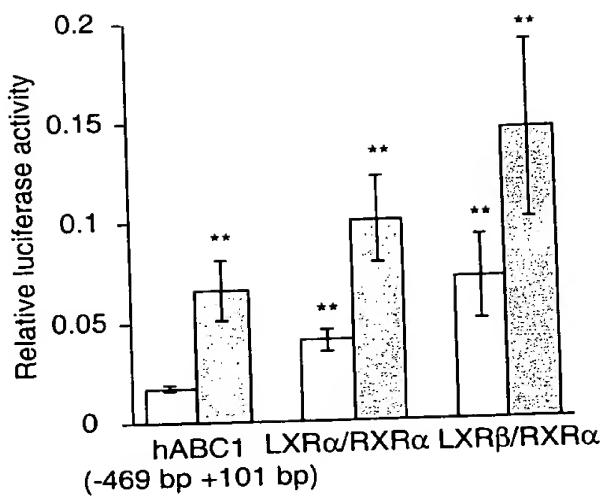


FIG. 6B



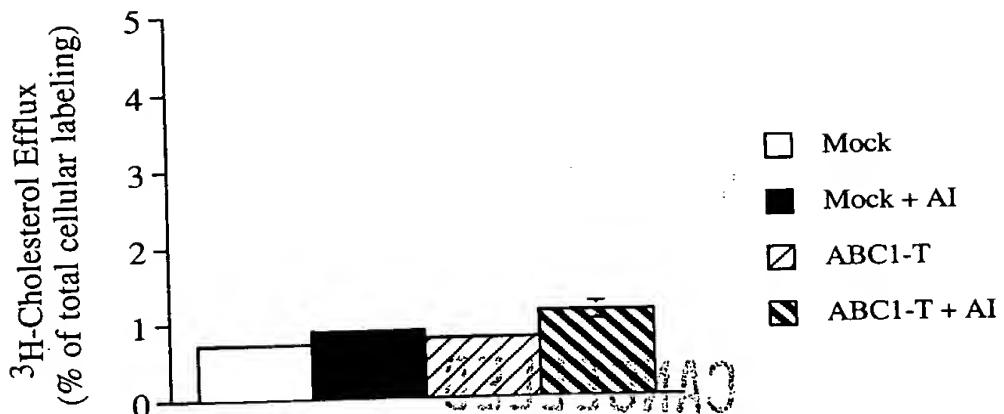
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FIG. 7



0082400 "22E09560

FIG. 8A



ABC1-T: 61 MPSAGT--- (Genebank Accession: X75926; the methionine 61 here was originally designated as the start methionine. This version of cDNA is inactive in stimulating cholesterol efflux.)

FIG. 8B

